

Package ‘BiocCheck’

October 18, 2022

Version 1.32.1

Title Bioconductor-specific package checks

Description BiocCheck guides maintainers through Bioconductor best practices. It runs Bioconductor-specific package checks by searching through package code, examples, and vignettes. Maintainers are required to address all errors, warnings, and most notes produced.

Depends R (>= 4.2.0)

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VignetteBuilder knitr

Imports biocViews (>= 1.33.7), BiocManager, stringdist, graph, httr, tools, codetools, methods, utils, knitr

Suggests RUnit, BiocGenerics, Biobase, jsonlite, rmarkdown, downloader, devtools (>= 1.4.1), usethis, BiocStyle

Enhances codetoolsBioC

biocViews Infrastructure

URL <https://github.com/Bioconductor/BiocCheck>

BugReports <https://github.com/Bioconductor/BiocCheck/issues>

RoxygenNote 7.1.2

git_url <https://git.bioconductor.org/packages/BiocCheck>

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BiocCheck	<i>Check a package's adherence with the Bioconductor Package Guidelines</i>
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Description

Analyzes an R package for adherence with Bioconductor package guidelines and best practices. The check outputs are categorized into ERROR, WARNING, and NOTE. See the vignette for more details. BiocCheck is complementary to R CMD check, which should always be run first.

Usage

```
BiocCheck(package = ".", checkDir = dirname(package), debug = FALSE, ...)
```

Arguments

package	A directory or tarball (.tar.gz file) of an R package.
checkDir	A directory where the BiocCheck output directory will go. By default, it will be placed in the same directory as the package directory.
debug	Whether to append the names of functions that correspond to each condition raised by BiocCheck in the written log (i.e., in the '<package_name>.BiocCheck' folder). This option is only relevant to developers and contributors to BiocCheck.
...	See the details section for available options. When running BiocCheck, options can be specified as: <code>BiocCheck(package, `no-check-vignettes`=TRUE)</code>

Details

BiocCheck() reviews R packages for adherence with Bioconductor package guidelines and best practices. See <https://contributions.bioconductor.org> for the latest guidance for writing Bioconductor software. Some rationale behind these best practices can be seen in the vignette and pages in the references section. The vignette also provides detailed explanations of all the checks performed by BiocCheck.

BiocCheck is called within R with

```
BiocCheck(<package>)
```

where package points to the source directory or the .tar.gz tarball that was created using R CMD build.

Note that BiocCheck is complementary to R CMD check. R CMD check should always be run first for best results.

... options:

- new-package** enable checks specific to new packages
- no-check-dependencies** disable check for bad dependencies
- no-check-deprecated** disable check for usage of deprecated packages
- no-check-remotes** disable check for usage of remote packages other than those hosted on CRAN or Bioconductor
- no-check-version-num** disable check for valid version number
- no-check-R-ver** disable check for valid R version
- no-check-pkg-size** disable check for package tarball size
- no-check-file-size** disable check for individual file size
- no-check-bioc-views** disable biocViews-specific checks (for non-BioC packages)
- no-check-bbs** disable BBS-specific checks (for non-BioC packages). Valid DESCRIPTION
- no-check-description** disable DESCRIPTION file checks
- no-check-namespace** disable namespace checks
- no-check-vignettes** disable vignette checks
- no-check-library-calls** disable check usage of functions that install or update packages
- no-check-install-self** disable check for require or library of itself
- no-check-coding-practices** disable check for some common best coding practices
- no-check-function-len** disable check for function length
- no-check-man-doc** disable checks for man page documentation
- no-check-news** disable checks for NEWS file
- no-check-unit-tests** disable checks for unit tests
- no-check-skip-bioc-tests** disable check for tests that skip when on bioc
- no-check-formatting** disable checks for file formatting
- no-check-CRAN** disable check for if package exists in CRAN
- no-check-bioc-help** disable check for registration on Bioconductor mailing list and support site
- build-output-file** file containing R CMD build output, for additional analysis
- quit-with-status** enable exit code option when performing check

Value

Mostly called for the side effect of the information displayed. When called interactively, returns a list with three components:

ERROR	Items that must be fixed before the package can be accepted into Bioconductor.
WARNING	We strongly suggest fixing these items.
NOTE	Fixing these items is not required, there is no expectation that considerations will escalate in severity.

Author(s)

Dan Tenenbaum, Lori Shepherd, and Marcel Ramos

References

<https://contributions.bioconductor.org>

Examples

```
packageDir <- system.file("testpackages", "testpkg0", package="BiocCheck")
BiocCheck(packageDir, `quit-with-status`=FALSE)
```

BiocCheckGitClone *Checks specific to a Git clone of a package repository*

Description

Analyzes an R package for adherence with Bioconductor package guidelines and best practices. The check outputs are categorized into ERROR, WARNING, and NOTE. This function is typically used in the Bioconductor Build System (BBS) and not intended for general use.

Usage

```
BiocCheckGitClone(package=".", ...)
```

Arguments

package	A directory containing an R source package. Not a package tar ball.
...	Currently, only <code>quit-with-status</code> is available. See <code>BiocCheck</code>

Details

`BiocCheckGitClone()` reviews R packages for adherence with Bioconductor package guidelines and best practices. See <https://contributions.bioconductor.org> for the latest guidance for writing Bioconductor software. This function should only be run on a source directory and not on a tarball.

`BiocCheckGitClone` is called within R with, as

```
BiocCheckGitClone(<package>)
```

where `package` is the source directory containing the R package.

Value

Mostly called for the side effect of the information displayed. When called interactively, returns a list with three components:

ERROR	Items that must be fixed before the package can be accepted into Bioconductor.
WARNING	We strongly suggest fixing these items.
NOTE	Fixing these items is not required, there is no expectation that considerations will escalate in severity.

Author(s)

Lori Shepherd

References

<https://contributions.bioconductor.org>

Examples

```
packageDir <- system.file("testpackages", "testpkg0", package="BiocCheck")
BiocCheckGitClone(packageDir, `quit-with-status`=FALSE)
```

Context	<i>Report context of events to user with a data.frame of events and locations</i>
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Description

Report context of events to user with a data.frame of events and locations

Usage

```
Context(pkg = "", file = "", lines = character(), idx = logical())
```

Arguments

pkg	character(1) name of the package
file	character(1) full path (including package name) of file being summarized.
lines	character() vector of text lines in file
idx	logical() same length as lines indicating lines in which event occurs

Value

Context: a data.frame() with columns File, Line, and Context

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